

Genome-wide association studies

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 An abbreviated version of this protocol was published in eLIFE in May 2021

Genetic variation, environment and demography intersect to shape Arabidopsis defense metabolite variation across Europe

DOI: 10.7554/eLife.67784

Detailed protocol

As all the GWAS are with Arabidopsis accessions we did the GWAS using the 1001 genomes tool (easyGWAS <https://easygwas.ethz.ch/>).

We used the EMMAX algorithm, MAF=0.05.

We used the amounts of each glucosinolate as a trait for each GWAS.

Please let us know if there is anything else we can help with.

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Katz, E. and Kliebenstein, D. (2022). Genome-wide association studies. Bio-protocol Preprint. bio-protocol.org/prep1546.
2. Katz, E., Li, J., Jaegle, B., Ashkenazy, H., Abrahams, S. R., Bagaza, C., Holden, S., Pires, C. J., Angelovici, R. and Kliebenstein, D. J. (2021). Genetic variation, environment and demography intersect to shape Arabidopsis defense metabolite variation across Europe. eLIFE. DOI: [10.7554/eLife.67784](https://doi.org/10.7554/eLife.67784)

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